

SEQUENCE LISTING

<110> Levinson, Douglas A.
Lloyd, Clare M.
McCarthy, Sean A.

<120> COMPOSITIONS AND METHODS FOR THE TREATMENT AND
DIAGNOSIS OF IMMUNE DISORDERS

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<140> 09/324,986

<141> 1999-06-02

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<150> 08/609,583

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 Gln Gln Glu Asp Leu Gly Thr Ala Glu Phe Gly Glu Thr Pro Phe Ser
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 gac ctc aca gag gag gag ttt ggc cag tta tac ggg cag gag agg tca 339
 Asp Leu Thr Glu Glu Glu Phe Gly Gln Leu Tyr Gly Gln Glu Arg Ser
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 Pro Glu Arg Thr Pro Asn Met Thr Lys Lys Val Glu Ser Asn Thr Trp
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Glu Lys Glu Gly Met Gln Thr Gly Thr Val Leu Ser His Ser Arg Lys	
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Ser Glu Lys Asp Tyr Pro Phe Gln Gly Asp Arg Lys Pro His Arg Cys
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Leu Ala Lys Lys Tyr Lys Lys Val Ala Trp Ile Gln Asp Phe Thr Met
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Leu Ser Asn Asn Glu Gln Ala Ile Ala His Tyr Leu Ala Val His Gly
245 250 255

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 1 5 10 15
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 20 25 30
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 35 40 45
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 50 55 60
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 65 70 75 80
 Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu
 85 90 95
 Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly
 100 105 110
 Ala Leu Met Arg Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp
 115 120 125
 Glu Glu
 130

<210> 15
 <211> 110
 <212> PRT
 <213> Mus musculus

<400> 15
 Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser
 1 5 10 15
 Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala
 20 25 30
 Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala
 35 40 45
 Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly
 50 55 60
 Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly
 65 70 75 80
 Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly
 85 90 95

Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
 100 105 110

<210> 16
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 16
 Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly Phe Trp
 1 5 10 15

Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly
 20 25 30

Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val
 35 40 45

Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val
 50 55 60

Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly
 65 70 75 80

Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr
 85 90 95

His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
 100 105

<210> 17
 <211> 122
 <212> PRT
 <213> Mus musculus

<400> 17
 Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
 1 5 10 15

Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
 20 25 30

Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Met Ala Ala Val Pro
 35 40 45

Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser
 50 55 60

Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly
 65 70 75 80

Gly Val Ala Ser Gly Ser Leu Val Gly Thr Leu Gln Ser Leu Gly Ala
 85 90 95

Thr Gly Leu Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser
 100 105 110

Ala Ile Ala Ala Val Ile Ala Arg Phe Tyr
115 120

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
ttgccataga gagacctc 18

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
tgctgtccaa ttatacagg 19

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
gaacacggca ttgtcactaa ct 22

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
cctcatagat gggcactgtg t 21

<210> 22
<211> 843
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

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 actctaccta catctgggac acttgtgcct atgtgctggg gcaagggatt ctgtccttgg 180
 tcacagtgtg ccaatgagtt gctcagaact gatgaaagaa atgtgacata tcagaaatcc 240
 agcagatacc agctaaaggg cgatctcaac aaaggagatg tgtctctgat cataaagaat 300
 gtgactctgg atgaccatgg gacctactgc tgcaggatac agttccctgg tcttatgaat 360
 gataaaaaat tagaactgaa attagacatc aaagcagcca aggtcactcc agtcagact 420
 gcccatgggg actctactac agcttctcca agaaccctaa ccacggagag aaatgggttca 480
 gagacacaga cactggtgac cctccataat aacaatggaa caaaaatttc cacatgggct 540
 gatgaaatta aggactctgg agaaacgata agaactgcta tccacattgg agtgggagtc 600
 tctgctgggt tgaccctggc acttatcatt ggtgtcttaa tccttaaagtg gtattcctgt 660
 aagaaaaaga agttatcgag tttgagcctt attacactgg ccaacttgcc tccaggaggg 720
 ttggcaaagtg caggagcagt caggattcgc tctgaggaaa atatctacac catcgaggag 780
 aacgtatatg aagtggagaa ttcaaagag tactactgct acgtcaacag ccagcagcca 840
 tcc 843

<210> 23

<211> 2236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (42)..(944)

<400> 23

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 Met Phe Ser His Leu
 1 5
 ccc ttt gac tgt gtc ctg ctg ctg ctg ctg cta cta ctt aca agg tcc 104
 Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu Leu Leu Thr Arg Ser
 10 15 20
 tca gaa gtg gaa tac aga gcg gag gtc ggt cag aat gcc tat ctg ccc 152
 Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr Leu Pro
 25 30 35

tgc ttc tac acc cca gcc gcc cca ggg aac ctc gtg ccc gtc tgc tgg	200
Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val Cys Trp	
40 45 50	
ggc aaa gga gcc tgt cct gtg ttt gaa tgt ggc aac gtg gtg ctc agg	248
Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val Leu Arg	
55 60 65	
act gat gaa agg gat gtg aat tat tgg aca tcc aga tac tgg cta aat	296
Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp Leu Asn	
70 75 80 85	
ggg gat ttc cgc aaa gga gat gtg tcc ctg acc ata gag aat gtg act	344
Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr Ile Glu Asn Val Thr	
90 95 100	
cta gca gac agt ggg atc tac tgc tgc cgg atc caa atc cca ggc ata	392
Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro Gly Ile	
105 110 115	
atg aat gat gaa aaa ttt aac ctg aag ttg gtc atc aaa cca gcc aag	440
Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro Ala Lys	
120 125 130	
gtc acc cct gca ccg act ctg cag aga gac ttc act gca gcc ttt cca	488
Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe Thr Ala Ala Phe Pro	
135 140 145	
agg atg ctt acc acc agg gga cat ggc cca gca gag aca cag aca ctg	536
Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala Glu Thr Gln Thr Leu	
150 155 160 165	
ggg agc ctc cct gat ata aat cta aca caa ata tcc aca ttg gcc aat	584
Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile Ser Thr Leu Ala Asn	
170 175 180	
gag tta cgg gac tct aga ttg gcc aat gac tta cgg gac tct gga gca	632
Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu Arg Asp Ser Gly Ala	
185 190 195	
acc atc aga ata ggc atc tac atc gga gca ggg atc tgt gct ggg ctg	680
Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly Ile Cys Ala Gly Leu	
200 205 210	
gct ctg gct ctt atc ttc ggc gct tta att ttc aaa tgg tat tct cat	728
Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe Lys Trp Tyr Ser His	
215 220 225	
agc aaa gag aag ata cag aat tta agc ctc atc tct ttg gcc aac ctc	776
Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile Ser Leu Ala Asn Leu	
230 235 240 245	
cct ccc tca gga ttg gca aat gca gta gca gag gga att cgc tca gaa	824
Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu Gly Ile Arg Ser Glu	
250 255 260	

gaa aac atc tat acc att gaa gag aac gta tat gaa gtg gag gag ccc 872
 Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Glu Pro
 265 270 275

aat gag tat tat tgc tat gtc agc agc agg cag caa ccc tca caa cct 920
 Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln Gln Pro Ser Gln Pro
 280 285 290

ttg ggt tgt cgc ttt gca atg cca tagatccaac caccttattt ttgagcttgg 974
 Leu Gly Cys Arg Phe Ala Met Pro
 295 300

tgttttgtct ttttcagaaa ctatgagctg tgtcacctga ctggtttttg aggttctgtc 1034

cactgctatg gagcagagtt ttcccatttt cagaagataa tgactcacat gggaattgaa 1094

ctgggacctg cactgaactt aaacaggcat gtcattgcct ctgtatttaa gccaacagag 1154

ttaccaacc cagagactgt taatcatgga tgtagagct caaacgggct tttatataca 1214

ctaggaattc ttgacgtggg gtctctggag ctccaggaaa ttcgggcaca tcatatgtcc 1274

atgaaacttc agataaacta ggraaaactg ggtgctgagg tgaaagcata acttttttgg 1334

cacagaaagt ctaaaggggc cactgatttt caaagagatc tgtgatccct ttttgttttt 1394

tgtttttgag atggagtctt gctctgttgc ccaggctgga gtgcaatggc acaatctcgg 1454

ctcactgcaa gctccgctc ctgggttcaa gcgattctcc tgccctcagcc tcctgagtgg 1514

ctgggattac aggcattgcac caccatgccc agctaatttg ttgtattttt agtagagaca 1574

gggtttcacc atgttggcca gtgtggtctc aaactcctga cctcatgatt tgccctgcctc 1634

ggcctcccaa agcactggga ttacaggcgt gagccaccac atccagccag tgatccctaa 1694

aagattaaga gatgactgga ctaggtctac cttgatcttg aagattccct tggaatgttg 1754

agatttaggc ttatttgagc actacctgcc caactgtcag tgccagtgca tagcccttct 1814

tttgtctccc ttatgaagac tgccctgcag ggctgagatg tggcaggagc tcccagggaa 1874

aaaggaagtg catttgattg gtgtgtattg gccaaagttt gcttgttgtg tgcttgaaag 1934

aaaatatctc tgaccaactt ctgtattcgt ggaccaaact gaagctatat ttttcacaga 1994

agaagaagca gtgacgggga cacaaattct gttgcctggg ggaaagaagg caaaggcctt 2054

cagcaatcta tattaccagc gctggatcct ttgacagaga gtggtcccta aacttaaatt 2114

tcaagacggt ataggcttga tctgtcttgc ttattgttgc ccctgcgcc tagcacaatt 2174

ctgacacaca attggaactt actaaaaatt tttttttact gttaaaaaaa aaaaaaaaaa 2234

aa 2236

<210> 24

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 24

Met	Phe	Ser	His	Leu	Pro	Phe	Asp	Cys	Val	Leu	Leu	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Leu	Thr	Arg	Ser	Ser	Glu	Val	Glu	Tyr	Arg	Ala	Glu	Val	Gly	Gln	20	25	30	
Asn	Ala	Tyr	Leu	Pro	Cys	Phe	Tyr	Thr	Pro	Ala	Ala	Pro	Gly	Asn	Leu	35	40	45	
Val	Pro	Val	Cys	Trp	Gly	Lys	Gly	Ala	Cys	Pro	Val	Phe	Glu	Cys	Gly	50	55	60	
Asn	Val	Val	Leu	Arg	Thr	Asp	Glu	Arg	Asp	Val	Asn	Tyr	Trp	Thr	Ser	65	70	75	80
Arg	Tyr	Trp	Leu	Asn	Gly	Asp	Phe	Arg	Lys	Gly	Asp	Val	Ser	Leu	Thr	85	90	95	
Ile	Glu	Asn	Val	Thr	Leu	Ala	Asp	Ser	Gly	Ile	Tyr	Cys	Cys	Arg	Ile	100	105	110	
Gln	Ile	Pro	Gly	Ile	Met	Asn	Asp	Glu	Lys	Phe	Asn	Leu	Lys	Leu	Val	115	120	125	
Ile	Lys	Pro	Ala	Lys	Val	Thr	Pro	Ala	Pro	Thr	Leu	Gln	Arg	Asp	Phe	130	135	140	
Thr	Ala	Ala	Phe	Pro	Arg	Met	Leu	Thr	Thr	Arg	Gly	His	Gly	Pro	Ala	145	150	155	160
Glu	Thr	Gln	Thr	Leu	Gly	Ser	Leu	Pro	Asp	Ile	Asn	Leu	Thr	Gln	Ile	165	170	175	
Ser	Thr	Leu	Ala	Asn	Glu	Leu	Arg	Asp	Ser	Arg	Leu	Ala	Asn	Asp	Leu	180	185	190	
Arg	Asp	Ser	Gly	Ala	Thr	Ile	Arg	Ile	Gly	Ile	Tyr	Ile	Gly	Ala	Gly	195	200	205	
Ile	Cys	Ala	Gly	Leu	Ala	Leu	Ala	Leu	Ile	Phe	Gly	Ala	Leu	Ile	Phe	210	215	220	
Lys	Trp	Tyr	Ser	His	Ser	Lys	Glu	Lys	Ile	Gln	Asn	Leu	Ser	Leu	Ile	225	230	235	240
Ser	Leu	Ala	Asn	Leu	Pro	Pro	Ser	Gly	Leu	Ala	Asn	Ala	Val	Ala	Glu	245	250	255	
Gly	Ile	Arg	Ser	Glu	Glu	Asn	Ile	Tyr	Thr	Ile	Glu	Glu	Asn	Val	Tyr	260	265	270	
Glu	Val	Glu	Glu	Pro	Asn	Glu	Tyr	Tyr	Cys	Tyr	Val	Ser	Ser	Arg	Gln	275	280	285	

10004633-120404

Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
 290 295 300

<210> 25
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 25
 aaattttattc tcgaggaccc acgcgtccgg atttccc 37

<210> 26
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide oligonucleotide

<400> 26
 ttaatttgga tccccagttc tgatcgtttc tccagagtc 39

<210> 27
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 27
 aaattttattc tcgagcgcta acagaggtgt cc 32

<210> 28
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 28
 ttaatttgga tcccctctga tgggtgctcc agagtcccg 39

<210> 29
 <211> 31

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 29
ccgcgggtac cagtaaatacg tcctgggggtg g 31

<210> 30
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 30
aaataaagga tccctacatc cagcaactat gtagta 36

<210> 31
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 31
gcgcaattga ctagtgaccc acgcgtccgg atttc 35

<210> 32
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 32
gacgcggatc ctcaggatgg ctgctggctg 30

<210> 33
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 33
gaacacacta gtactatcct gtgccattgc catagaga 38

<210> 34
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 34
ggaatattgg gcccttggat cccaagtctg cacacctgca ctcc 44

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 35
gtaaatcgtc ctggggctctg g 21

<210> 36
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 36
ccttctgata acacaagcat aaatc 25

<210> 37
<211> 903
<212> DNA
<213> Homo sapiens

<400> 37
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tcctcagaag tggaatacag agcggaggtc ggtcagaatg cctatctgcc ctgcttctac 120
accccagccg ccccagggaa cctcgtgccc gtctgctggg gcaaaggagc ctgtcctgtg 180
tttgaatgtg gcaacgtggt gctcaggact gatgaaaggg atgtgaatta ttggacatcc 240
agatactggc taaatgggga tttccgcaaa ggagatgtgt ccctgaccat agagaatgtg 300

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actctagcag acagtgggat ctactgctgc cggatccaaa tcccaggcat aatgaatgat 360
gaaaaattta acctgaagtt ggtcatcaaa ccagccaagg tcaccctgc accgactctg 420
cagagagact tctctgcagc ctttccaagg atgcttacca ccaggggaca tggcccagca 480
gagacacaga cactggggag cctccctgat ataaatctaa cacaaatc cacttggtg 540
aatgagttac gggactctag attggccaat gacttacggg actctggagc aaccatcaga 600
ataggcatct acatcggagc agggatctgt gctgggctgg ctctggctct tatcttcggc 660
gctttaattt tcaaattgga ttctcatagc aaagagaaga tacagaattt aagcctcacc 720
tctttggcca acctccctcc ctcaggattg gcaaattgcag tagcagaggg aattcgctca 780
gaagaaaaca tctataccat tgaagagaac gtatatgaag tggaggagcc caatgagtat 840
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cca

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903

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<210> 38
<211> 1704
<212> DNA
<213> Mus musculus

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<220>
<221> CAAT_signal
<222> (1)..(1704)

<220>
<221> CDS
<222> (1)..(1701)

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<400> 38
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1 5 10 15

ctt ccc atg tat ttg aca gtt acg gag ggc agt aaa tcg tcc tgg ggt 96
Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
20 25 30

ctg gaa aat gag gct tta att gtg aga tgc ccc caa aga gga cgc tcg 144
Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
35 40 45

act tat cct gtg gaa tgg tat tac tca gat aca aat gaa agt att cct 192
Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
50 55 60

act caa aaa aga aat cgg atc ttt gtc tca aga gat cgt ctg aag ttt 240
Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
65 70 75 80

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cta cca gcc aga gtg gaa gac tct ggg att tat gct tgt gtt atc aga	288
Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg	
85 90 95	
agc ccc aac ttg aat aag act gga tac ttg aat gtc acc ata cat aaa	336
Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys	
100 105 110	
aag ccg cca agc tgc aat atc cct gat tat ttg atg tac tcg aca gta	384
Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val	
115 120 125	
cgt gga tca gat aaa aat ttc aag ata acg tgt cca aca att gac ctg	432
Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu	
130 135 140	
tat aat tgg aca gca cct gtt cag tgg ttt aag aac tgc aaa gct ctc	480
Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu	
145 150 155 160	
caa gag cca agg ttc agg gca cac agg tcc tac ttg ttc att gac aac	528
Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn	
165 170 175	
gtg act cat gat gat gaa ggt gac tac act tgt caa ttc aca cac gcg	576
Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala	
180 185 190	
gag aat gga acc aac tac atc gtg acg gcc acc aga tca ttc aca gtt	624
Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val	
195 200 205	
gaa gaa aaa ggc ttt tct atg ttt cca gta att aca aat cct cca tac	672
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr	
210 215 220	
aac cac aca atg gaa gtg gaa ata gga aaa cca gca agt att gcc tgt	720
Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys	
225 230 235 240	
tca gct tgc ttt ggc aaa ggc tct cac ttc ttg gct gat gtc ctg tgg	768
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp	
245 250 255	
cag att aac aaa aca gta gtt gga aat ttt ggt gaa gca aga att caa	816
Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln	
260 265 270	
gaa gag gaa ggt cga aat gaa agt tcc agc aat gac atg gat tgt tta	864
Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu	
275 280 285	
acc tca gtg tta agg ata act ggt gtg aca gaa aag gac ctg tcc ctg	912
Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu	
290 295 300	

gaa tat gac tgt ctg gcc ctg aac ctt cat ggc atg ata agg cac acc	960
Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr	
305 310 315 320	
ata agg ctg aga agg aaa caa cca att gat cac cga agc atc tac tac	1008
Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp His Arg Ser Ile Tyr Tyr	
325 330 335	
ata gtt gct gga tgt agt tta ttg cta atg ttt atc aat gtc ttg gtg	1056
Ile Val Ala Gly Cys Ser Leu Leu Leu Met Phe Ile Asn Val Leu Val	
340 345 350	
ata gtc tta aaa gtg ttc tgg att gag gtt gct ctg ttc tgg aga gat	1104
Ile Val Leu Lys Val Phe Trp Ile Glu Val Ala Leu Phe Trp Arg Asp	
355 360 365	
ata gtg aca cct tac aaa acc cgg aac gat ggc aag ctc tac gat gcg	1152
Ile Val Thr Pro Tyr Lys Thr Arg Asn Asp Gly Lys Leu Tyr Asp Ala	
370 375 380	
tac atc att tac cct cgg gtc ttc cgg ggc agc gcg gcg gga acc cac	1200
Tyr Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly Thr His	
385 390 395 400	
tct gtg gag tac ttt gtt cac cac act ctg ccc gac gtt ctt gaa aat	1248
Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu Glu Asn	
405 410 415	
aaa tgt ggc tac aaa ttg tgc att tat ggg aga gac ctg tta cct ggg	1296
Lys Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu Pro Gly	
420 425 430	
caa gat gca gcc acc gtg gtg gaa agc agt atc cag aat agc aga aga	1344
Gln Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser Arg Arg	
435 440 445	
cag gtg ttt gtt ctg gcc cct cac atg atg cac agc aag gaa ttt gcc	1392
Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu Phe Ala	
450 455 460	
tac gag cag gag att gct ctg cac agc gcc ctc atc cag aac aac tcc	1440
Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn Asn Ser	
465 470 475 480	
aag gtg att ctt att gaa atg gag cct ctg ggt gag gca agc cga cta	1488
Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser Arg Leu	
485 490 495	
cag gtt ggg gac ctg caa gat tct ctc cag cat ctt gtg aaa att cag	1536
Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys Ile Gln	
500 505 510	
ggg acc atc aag tgg agg gaa gat cat gtg gcc gac aag cag tct cta	1584
Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu	
515 520 525	

agt tcc aaa ttc tgg aag cat gtg agg tac caa atg cca gtg cca gaa 1632
 Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Glu
 530 535 540

aga gcc tcc aag acg gca tct gtt gcg gct ccg ttg agt ggc aag gca 1680
 Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly Lys Ala
 545 550 555 560

tgc tta gac ctg aaa cac ttt tga 1704
 Cys Leu Asp Leu Lys His Phe
 565

<210> 39
 <211> 567
 <212> PRT
 <213> Mus musculus

<400> 39
 Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
 1 5 10 15

Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
 20 25 30

Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
 35 40 45

Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
 50 55 60

Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
 65 70 75 80

Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
 85 90 95

Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
 100 105 110

Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
 115 120 125

Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
 130 135 140

Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
 145 150 155 160

Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
 165 170 175

Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
 180 185 190

Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
 195 200 205

10004633-120401

Glu	Glu	Lys	Gly	Phe	Ser	Met	Phe	Pro	Val	Ile	Thr	Asn	Pro	Pro	Tyr	210	215	220
Asn	His	Thr	Met	Glu	Val	Glu	Ile	Gly	Lys	Pro	Ala	Ser	Ile	Ala	Cys	225	230	235 240
Ser	Ala	Cys	Phe	Gly	Lys	Gly	Ser	His	Phe	Leu	Ala	Asp	Val	Leu	Trp	245	250	255
Gln	Ile	Asn	Lys	Thr	Val	Val	Gly	Asn	Phe	Gly	Glu	Ala	Arg	Ile	Gln	260	265	270
Glu	Glu	Glu	Gly	Arg	Asn	Glu	Ser	Ser	Ser	Asn	Asp	Met	Asp	Cys	Leu	275	280	285
Thr	Ser	Val	Leu	Arg	Ile	Thr	Gly	Val	Thr	Glu	Lys	Asp	Leu	Ser	Leu	290	295	300
Glu	Tyr	Asp	Cys	Leu	Ala	Leu	Asn	Leu	His	Gly	Met	Ile	Arg	His	Thr	305	310	315 320
Ile	Arg	Leu	Arg	Arg	Lys	Gln	Pro	Ile	Asp	His	Arg	Ser	Ile	Tyr	Tyr	325	330	335
Ile	Val	Ala	Gly	Cys	Ser	Leu	Leu	Leu	Met	Phe	Ile	Asn	Val	Leu	Val	340	345	350
Ile	Val	Leu	Lys	Val	Phe	Trp	Ile	Glu	Val	Ala	Leu	Phe	Trp	Arg	Asp	355	360	365
Ile	Val	Thr	Pro	Tyr	Lys	Thr	Arg	Asn	Asp	Gly	Lys	Leu	Tyr	Asp	Ala	370	375	380
Tyr	Ile	Ile	Tyr	Pro	Arg	Val	Phe	Arg	Gly	Ser	Ala	Ala	Gly	Thr	His	385	390	395 400
Ser	Val	Glu	Tyr	Phe	Val	His	His	Thr	Leu	Pro	Asp	Val	Leu	Glu	Asn	405	410	415
Lys	Cys	Gly	Tyr	Lys	Leu	Cys	Ile	Tyr	Gly	Arg	Asp	Leu	Leu	Pro	Gly	420	425	430
Gln	Asp	Ala	Ala	Thr	Val	Val	Glu	Ser	Ser	Ile	Gln	Asn	Ser	Arg	Arg	435	440	445
Gln	Val	Phe	Val	Leu	Ala	Pro	His	Met	Met	His	Ser	Lys	Glu	Phe	Ala	450	455	460
Tyr	Glu	Gln	Glu	Ile	Ala	Leu	His	Ser	Ala	Leu	Ile	Gln	Asn	Asn	Ser	465	470	475 480
Lys	Val	Ile	Leu	Ile	Glu	Met	Glu	Pro	Leu	Gly	Glu	Ala	Ser	Arg	Leu	485	490	495
Gln	Val	Gly	Asp	Leu	Gln	Asp	Ser	Leu	Gln	His	Leu	Val	Lys	Ile	Gln	500	505	510

Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu
515 520 525

Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Glu
530 535 540

Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly Lys Ala
545 550 555 560

Cys Leu Asp Leu Lys His Phe
565

<210> 40
<211> 1029
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1026)

<400> 40
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Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
1 5 10 15

ctt ccc atg tat ttg aca gtt acg gag ggc agt aaa tcg tcc tgg ggt 96
Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
20 25 30

ctg gaa aat gag gct tta att gtg aga tgc ccc caa aga gga cgc tcg 144
Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
35 40 45

act tat cct gtg gaa tgg tat tac tca gat aca aat gaa agt att cct 192
Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
50 55 60

act caa aaa aga aat cgg atc ttt gtc tca aga gat cgt ctg aag ttt 240
Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
65 70 75 80

cta cca gcc aga gtg gaa gac tct ggg att tat gct tgt gtt atc aga 288
Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
85 90 95

agc ccc aac ttg aat aag act gga tac ttg aat gtc acc ata cat aaa 336
Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
100 105 110

aag ccg cca agc tgc aat atc cct gat tat ttg atg tac tcg aca gta 384
Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
115 120 125

cgt gga tca gat aaa aat ttc aag ata acg tgt cca aca att gac ctg 432
Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
130 135 140

tat aat tgg aca gca cct gtt cag tgg ttt aag aac tgc aaa gct ctc	480
Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu	
145 150 155 160	
caa gag cca agg ttc agg gca cac agg tcc tac ttg ttc att gac aac	528
Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn	
165 170 175	
gtg act cat gat gat gaa ggt gac tac act tgt caa ttc aca cac gcg	576
Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala	
180 185 190	
gag aat gga acc aac tac atc gtg acg gcc acc aga tca ttc aca gtt	624
Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val	
195 200 205	
gaa gaa aaa ggc ttt tct atg ttt cca gta att aca aat cct cca tac	672
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr	
210 215 220	
aac cac aca atg gaa gtg gaa ata gga aaa cca gca agt att gcc tgt	720
Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys	
225 230 235 240	
tca gct tgc ttt ggc aaa ggc tct cac ttc ttg gct gat gtc ctg tgg	768
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp	
245 250 255	
cag att aac aaa aca gta gtt gga aat ttt ggt gaa gca aga att caa	816
Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln	
260 265 270	
gaa gag gaa ggt cga aat gaa agt tcc agc aat gac atg gat tgt tta	864
Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu	
275 280 285	
acc tca gtg tta agg ata act ggt gtg aca gaa aag gac ctg tcc ctg	912
Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu	
290 295 300	
gaa tat gac tgt ctg gcc ctg aac ctt cat ggc atg ata agg cac acc	960
Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr	
305 310 315 320	
ata agg ctg aga agg aaa caa cca att gat cac cga agc atc tac tac	1008
Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp His Arg Ser Ile Tyr Tyr	
325 330 335	
ata gtt gct gga tgt agt tga	1029
Ile Val Ala Gly Cys Ser	
340	

<210> 41

<211> 342

<212> PRT

<213> Mus musculus

<400> 41

Met	Ile	Asp	Arg	Gln	Arg	Met	Gly	Leu	Trp	Ala	Leu	Ala	Ile	Leu	Thr	1	5	10	15
Leu	Pro	Met	Tyr	Leu	Thr	Val	Thr	Glu	Gly	Ser	Lys	Ser	Ser	Trp	Gly	20	25	30	
Leu	Glu	Asn	Glu	Ala	Leu	Ile	Val	Arg	Cys	Pro	Gln	Arg	Gly	Arg	Ser	35	40	45	
Thr	Tyr	Pro	Val	Glu	Trp	Tyr	Tyr	Ser	Asp	Thr	Asn	Glu	Ser	Ile	Pro	50	55	60	
Thr	Gln	Lys	Arg	Asn	Arg	Ile	Phe	Val	Ser	Arg	Asp	Arg	Leu	Lys	Phe	65	70	75	80
Leu	Pro	Ala	Arg	Val	Glu	Asp	Ser	Gly	Ile	Tyr	Ala	Cys	Val	Ile	Arg	85	90	95	
Ser	Pro	Asn	Leu	Asn	Lys	Thr	Gly	Tyr	Leu	Asn	Val	Thr	Ile	His	Lys	100	105	110	
Lys	Pro	Pro	Ser	Cys	Asn	Ile	Pro	Asp	Tyr	Leu	Met	Tyr	Ser	Thr	Val	115	120	125	
Arg	Gly	Ser	Asp	Lys	Asn	Phe	Lys	Ile	Thr	Cys	Pro	Thr	Ile	Asp	Leu	130	135	140	
Tyr	Asn	Trp	Thr	Ala	Pro	Val	Gln	Trp	Phe	Lys	Asn	Cys	Lys	Ala	Leu	145	150	155	160
Gln	Glu	Pro	Arg	Phe	Arg	Ala	His	Arg	Ser	Tyr	Leu	Phe	Ile	Asp	Asn	165	170	175	
Val	Thr	His	Asp	Asp	Glu	Gly	Asp	Tyr	Thr	Cys	Gln	Phe	Thr	His	Ala	180	185	190	
Glu	Asn	Gly	Thr	Asn	Tyr	Ile	Val	Thr	Ala	Thr	Arg	Ser	Phe	Thr	Val	195	200	205	
Glu	Glu	Lys	Gly	Phe	Ser	Met	Phe	Pro	Val	Ile	Thr	Asn	Pro	Pro	Tyr	210	215	220	
Asn	His	Thr	Met	Glu	Val	Glu	Ile	Gly	Lys	Pro	Ala	Ser	Ile	Ala	Cys	225	230	235	240
Ser	Ala	Cys	Phe	Gly	Lys	Gly	Ser	His	Phe	Leu	Ala	Asp	Val	Leu	Trp	245	250	255	
Gln	Ile	Asn	Lys	Thr	Val	Val	Gly	Asn	Phe	Gly	Glu	Ala	Arg	Ile	Gln	260	265	270	
Glu	Glu	Glu	Gly	Arg	Asn	Glu	Ser	Ser	Ser	Asn	Asp	Met	Asp	Cys	Leu	275	280	285	
Thr	Ser	Val	Leu	Arg	Ile	Thr	Gly	Val	Thr	Glu	Lys	Asp	Leu	Ser	Leu	290	295	300	

Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
305 310 315 320

Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp His Arg Ser Ile Tyr Tyr
325 330 335

Ile Val Ala Gly Cys Ser
340

<210> 42
<211> 606
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(603)

<400> 42
aga gat ata gtg aca cct tac aaa acc cgg aac gat ggc aag ctc tac 48
Arg Asp Ile Val Thr Pro Tyr Lys Thr Arg Asn Asp Gly Lys Leu Tyr
1 5 10 15
gat gcg tac atc att tac cct cgg gtc ttc cgg ggc agc gcg gcg gga 96
Asp Ala Tyr Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly
20 25 30
acc cac tct gtg gag tac ttt gtt cac cac act ctg ccc gac gtt ctt 144
Thr His Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu
35 40 45
gaa aat aaa tgt ggc tac aaa ttg tgc att tat ggg aga gac ctg tta 192
Glu Asn Lys Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu
50 55 60
cct ggg caa gat gca gcc acc gtg gtg gaa agc agt atc cag aat agc 240
Pro Gly Gln Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser
65 70 75 80
aga aga cag gtg ttt gtt ctg gcc cct cac atg atg cac agc aag gaa 288
Arg Arg Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu
85 90 95
ttt gcc tac gag cag gag att gct ctg cac agc gcc ctc atc cag aac 336
Phe Ala Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn
100 105 110
aac tcc aag gtg att ctt att gaa atg gag cct ctg ggt gag gca agc 384
Asn Ser Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser
115 120 125
cga cta cag gtt ggg gac ctg caa gat tct ctc cag cat ctt gtg aaa 432
Arg Leu Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys
130 135 140

10004633-120401

att cag ggg acc atc aag tgg agg gaa gat cat gtg gcc gac aag cag 480
 Ile Gln Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln
 145 150 155 160

tct cta agt tcc aaa ttc tgg aag cat gtg agg tac caa atg cca gtg 528
 Ser Leu Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val
 165 170 175

cca gaa aga gcc tcc aag acg gca tct gtt gcg gct ccg ttg agt ggc 576
 Pro Glu Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly
 180 185 190

aag gca tgc tta gac ctg aaa cac ttt tga 606
 Lys Ala Cys Leu Asp Leu Lys His Phe
 195 200

<210> 43
 <211> 201
 <212> PRT
 <213> Mus musculus

<400> 43
 Arg Asp Ile Val Thr Pro Tyr Lys Thr Arg Asn Asp Gly Lys Leu Tyr
 1 5 10 15

Asp Ala Tyr Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly
 20 25 30

Thr His Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu
 35 40 45

Glu Asn Lys Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu
 50 55 60

Pro Gly Gln Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser
 65 70 75 80

Arg Arg Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu
 85 90 95

Phe Ala Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn
 100 105 110

Asn Ser Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser
 115 120 125

Arg Leu Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys
 130 135 140

Ile Gln Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln
 145 150 155 160

Ser Leu Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val
 165 170 175

Pro Glu Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly
 180 185 190

10004633-120404

Lys Ala Cys Leu Asp Leu Lys His Phe
195 200

<210> 44
<211> 1357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (47) .. (1030)

<400> 44
atctcaacaa cgagttacca atacttgctc ttgattgata aacaga atg ggg ttt 55
Met Gly Phe
1

tgg atc tta gca att ctc aca att ctc atg tat tcc aca gca gca aag 103
Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr Ala Ala Lys
5 10 15

ttt agt aaa caa tca tgg ggc ctg gaa aat gag gct tta att gta aga 151
Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val Arg
20 25 30 35

tgt cct aga caa gga aaa cct agt tac acc gtg gat tgg tat tac tca 199
Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp Tyr Tyr Ser
40 45 50

caa aca aac aaa agt att ccc act cag gaa aga aat cgt gtg ttt gcc 247
Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg Val Phe Ala
55 60 65

tca ggc caa ctt ctg aag ttt cta cca gct gaa gtt gct gat tct ggt 295
Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala Asp Ser Gly
70 75 80

att tat acc tgt att gtc aga agt ccc aca ttc aat agg act gga tat 343
Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg Thr Gly Tyr
85 90 95

gcg aat gtc acc ata tat aaa aaa caa tca gat tgc aat gtt cca gat 391
Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn Val Pro Asp
100 105 110 115

tat ttg atg tat tca aca gta tct gga tca gaa aaa aat tcc aaa att 439
Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn Ser Lys Ile
120 125 130

tat tgt cct acc att gac ctc tac aac tgg aca gca cct ctt gag tgg 487
Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro Leu Glu Trp
135 140 145

ttt aag aat tgt cag gct ctt caa gga tca agg tac agg gcg cac aag 535
Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg Ala His Lys
150 155 160

10004633-120401

tca ttt ttg gtc att gat aat gtg atg act gag gac gca ggt gat tac	583
Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala Gly Asp Tyr	
165 170 175	
acc tgt aaa ttt ata cac aat gaa aat gga gcc aat tat agt gtg acg	631
Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr Ser Val Thr	
180 185 190 195	
gcg acc agg tcc ttc acg gtc aag gat gag caa ggc ttt tct ctg ttt	679
Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe Ser Leu Phe	
200 205 210	
cca gta atc gga gcc cct gca caa aat gaa ata aag gaa gtg gaa att	727
Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu Val Glu Ile	
215 220 225	
gga aaa aac gca aac cta act tgc tct gct tgt ttt gga aaa ggc act	775
Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly Lys Gly Thr	
230 235 240	
cag ttc ttg gct gcc gtc ctg tgg cag ctt aat gga aca aaa att aca	823
Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr Lys Ile Thr	
245 250 255	
gac ttt ggt gaa cca aga att caa caa gag gaa ggg caa aat caa agt	871
Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln Asn Gln Ser	
260 265 270 275	
ttc agc aat ggg ctg gct tgt cta gac atg gtt tta aga ata gct gac	919
Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg Ile Ala Asp	
280 285 290	
gtg aag gaa gag gat tta ttg ctg cag tac gac tgt ctg gcc ctg aat	967
Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu Ala Leu Asn	
295 300 305	
ttg cat ggc ttg aga agg cac acc gta aga cta agt agg aaa aat cca	1015
Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg Lys Asn Pro	
310 315 320	
agt aag gag tgt ttc tgagactttg atcacctgaa ctttctctag caagtgtgtaag	1070
Ser Lys Glu Cys Phe	
325	
cagaatggag tgtggttcca agagatccat caagacaatg ggaatggcct gtgccataaa	1130
atgtgcttct cttcttcggg atgttggttg ctgtctgac tttgtagact gttcctgttt	1190
gctgggagct tctctgctgc ttaaattggt cgctcctccc cactcctcc tatcgttggt	1250
ttgtctagaa cactcagctg cttcttttgggt catccttggt ttctaacttt atgaactccc	1310
tctgtgtcac tgtatgtgaa aggaaatgca ccaacaaccg aaaactg	1357
<210> 45	
<211> 328	
<212> PRT	

<213> Homo sapiens

<400> 45

Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
1 5 10 15

Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
20 25 30

Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
35 40 45

Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
50 55 60

Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala
65 70 75 80

Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
85 90 95

Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
100 105 110

Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
115 120 125

Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
130 135 140

Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145 150 155 160

Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
165 170 175

Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
180 185 190

Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe
195 200 205

Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu
210 215 220

Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly
225 230 235 240

Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr
245 250 255

Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln
260 265 270

Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg
275 280 285

10004633-10404

Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu
 290 295 300

Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg
 305 310 315 320

Lys Asn Pro Ser Lys Glu Cys Phe
 325

<210> 46

<211> 72

<212> DNA

<213> Mus musculus

<400> 46

ttattgctaa tgtttatcaa tgtcttggtg atagtcttaa aagtgttctg gattgaggtt 60

gctctgttct gg

72

<210> 47

<211> 1011

<212> DNA

<213> Mus musculus

<400> 47

atgattgaca gacagagaat gggactttgg gctttggcaa ttctgacact tcccatgtat 60
 ttgacagtta cggagggcag taaatcgctc tggggctctg aaaatgaggc ttttaattgtg 120
 agatgcccc aaagaggacg ctcgacttat cctgtggaat ggtattactc agatacaaat 180
 gaaagtattc ctactcaaaa aagaaatcgg atctttgtct caagagatcg tctgaagttt 240
 ctaccagcca gagtcgaaga ctctgggatt tatgcttgtg ttatcagaag ccccaacttg 300
 aataagactg gatacttgaa tgtcaccata cataaaaagc cgccaagctg caatatccct 360
 gattatttga tgtactcgac agtacgtgga tcagataaaa atttcaagat aagctgtcca 420
 acaattgacc tgtataattg gacagcacct gtccagtggg ttaagaactg caaagctctc 480
 caagagccaa gggttcaggc acacaggctc tacttggtca ttgacaacgt gactcatgat 540
 gatgaagggtg actacacttg tcaattcaca cagcgggaga atggaaccaa ctacatcgtg 600
 acggccacca gatcattcac agttgaagaa aaaggctttt ctatgtttcc agtaattaca 660
 aatcctccat acaaccacac aatggaagtg gaaataggaa aaccagcaag tattgcctgt 720
 tcagcttgct ttggcaaagg ctctcacttc ttggctgatg tcctgtggca gattaacaaa 780
 acagtagttg gaaatttttg tgaagcaaga attcaagaag aggaaggctg aaatgaaagt 840
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 <211> 337
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 Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
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 Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
 20 25 30
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 35 40 45
 Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
 50 55 60
 Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
 65 70 75 80
 Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
 85 90 95
 Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
 100 105 110
 Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
 115 120 125
 Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
 130 135 140
 Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
 145 150 155 160
 Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
 165 170 175
 Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
 180 185 190
 Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
 195 200 205
 Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
 210 215 220
 Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
 225 230 235 240
 Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
 245 250 255

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Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
260 265 270

Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
275 280 285

Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
290 295 300

Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
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Ile Arg Leu Arg Arg Lys Gln Pro Ser Lys Glu Cys Pro Ser His Ile
325 330 335

Ala

<210> 49

<211> 337

<212> PRT

<213> Mus musculus

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Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
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Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
20 25 30

Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
35 40 45

Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
50 55 60

Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
65 70 75 80

Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
85 90 95

Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
100 105 110

Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
115 120 125

Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
130 135 140

Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
145 150 155 160

Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
165 170 175

Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
180 185 190

Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
195 200 205

Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
210 215 220

Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
225 230 235 240

Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
245 250 255

Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
260 265 270

Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
275 280 285

Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
290 295 300

Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
305 310 315 320

Ile Arg Leu Arg Arg Lys Gln Pro Ser Lys Glu Cys Pro Ser His Ile
325 330 335

Ala

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